

0207/0202  
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## RAW SEQUENCE LISTING

DATE: 02/07/2002

PATENT APPLICATION: US/10/036,869

TIME: 11:11:06

Input Set : N:\Crf3\RULE60\10036869.raw

Output Set: N:\CRF3\02072002\J036869.raw

## SEQUENCE LISTING

## 3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Mixson, James A

7 (ii) TITLE OF INVENTION: CARRIER:DNA COMPLEXES CONTAINING DNA

8 ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN GENE  
9 THERAPY

11 (iii) NUMBER OF SEQUENCES: 43

13 (iv) CORRESPONDENCE ADDRESS:

14 (A) ADDRESSEE: Connolly, Bove, Lodge, &amp; Hutz

15 (B) STREET: 1220 Market Street, P.O. Box 2207

16 (C) CITY: Wilmington

17 (D) STATE: Delaware

18 (E) COUNTRY: U.S.A.

19 (F) ZIP: 19899

21 (v) COMPUTER READABLE FORM:

22 (A) MEDIUM TYPE: Floppy disk

23 (B) COMPUTER: IBM PC compatible

24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

27 (vi) CURRENT APPLICATION DATA:

C--&gt; 28 (A) APPLICATION NUMBER: US/10/036,869

C--&gt; 29 (B) FILING DATE: 29-Nov-2001

30 (C) CLASSIFICATION:

32 (vii) PRIOR APPLICATION DATA:

34 (A) APPLICATION NUMBER: US/08/985,526

35 (B) FILING DATE:

38 (A) APPLICATION NUMBER: US 08/608,845

39 (B) FILING DATE: 16-JUL-1996

41 (viii) ATTORNEY/AGENT INFORMATION:

42 (A) NAME: McMorro Jr., Robert G

44 (ix) TELECOMMUNICATION INFORMATION:

45 (A) TELEPHONE: (302) 658-9141

46 (B) TELEFAX: (302) 658-5613

48 (2) INFORMATION FOR SEQ ID NO: 1:

50 (i) SEQUENCE CHARACTERISTICS:

51 (A) LENGTH: 218 amino acids

52 (B) TYPE: amino acid

53 (D) TOPOLOGY: linear

59 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

61 Met Thr Glu Glu Asn Lys Glu Leu Ala Asn Glu Leu Arg Arg Pro Pro

62 1 5 10 15

64 Leu Cys Tyr His Asn Gly Val Gln Tyr Arg Asn Asn Glu Glu Trp Thr

65 20 25 30

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67   Val Asp Ser Cys Thr Glu Cys His Cys Gln Asn Ser Val Thr Ile Cys
68           35                      40                      45
70   Lys Lys Val Ser Cys Pro Ile Met Pro Cys Ser Asn Ala Thr Val Pro
71           50                      55                      60
73   Asp Gly Glu Cys Cys Pro Arg Cys Trp Pro Ser Asp Ser Ala Asp Asp
74           65                      70                      75                      80
76   Gly Trp Ser Pro Trp Ser Glu Trp Thr Ser Cys Ser Thr Ser Cys Gly
77           85                      90                      95
79   Asn Gly Ile Gln Gln Arg Gly Arg Ser Cys Asp Ser Leu Asn Asn Arg
80           100                     105                     110
82   Cys Glu Gly Ser Ser Val Gln Thr Arg Thr Cys His Ile Gln Glu Cys
83           115                     120                     125
85   Asp Lys Arg Phe Lys Gln Asp Gly Gly Trp Ser His Trp Ser Pro Trp
86           130                     135                     140
88   Ser Ser Cys Ser Val Thr Cys Gly Asp Gly Val Ile Thr Arg Ile Thr
89           145                     150                     155                     160
91   Asn Leu Cys Ser Pro Ser Pro Gln Met Asn Gly Lys Pro Cys Glu Gly
92           165                     170                     175
94   Arg Glu Ala Glu Thr Lys Ala Cys Lys Lys Asp Ala Cys Pro Ile Asn
95           180                     185                     190
97   Gly Gly Trp Gly Pro Trp Ser Pro Trp Asp Ile Cys Ser Val Thr Cys
98           195                     200                     205
100  Gly Gly Gly Val Gln Lys Arg Ser Arg Leu
101           210                     215
103 (2) INFORMATION FOR SEQ ID NO: 2:
105   (i) SEQUENCE CHARACTERISTICS:
106       (A) LENGTH: 657 base pairs
107       (B) TYPE: nucleic acid
108       (C) STRANDEDNESS: single
109       (D) TOPOLOGY: linear
115   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
117 ATGACTGAAG AGAACAAAGA GTTGGCCAAT GAGCTGAGGC GGCCTCCCCT ATGCTATCAC      60
119 AACGGAGTTC AGTACAGAAA TAACGAGGAA TGGACTGTTG ATAGCTGCAC TGAGTGTCCAC      120
121 TGTCAGAACT CAGTTACCAT CTGCAAAAAG GTGTCCTGCC CCATCATGCC CTGCTCCAAT      180
123 GCCACAGTTC CTGATGGAGA ATGCTGTCCT CGCTGTTGGC CCAGCGACTC TGCGGACGAT      240
125 GGCTGGTCTC CATGGTCCGA GTGGACCTCC TGTTCTACGA GCTGTGGCAA TGGAATTCAG      300
127 CAGCGCGGCC GTCCTGCGA TAGCCTCAAC AACCAGATGT AGGGCTCCTC GGTCCAGACA      360
128 CGGACCTGCC ACATTCAGGA GTGTGACAAA AGATTAAAC AGGATGGTGG CTGGAGCCAC      420
130 TGGTCCCCGT GGTCATCTTG TTCTGTGACA TGTGGTGATG GTGTGATCAC AAGGATCCGG      480
132 CTCTGCAACT CTCCCAGCCC CCAGATGAAT GGGAAACCCT GTGAAGGCGA AGCGCGGGAG      540
134 ACCAAAGCCT GCAAGAAAGA CGCCTGCCCC ATCAATGGAG GCTGGGGTCC TTGGTCACCA      600
136 TGGGACATCT GTTCTGTAC CTGTGGAGGA GGGGTACAGA AACGTAGTCG TCTCTAA      657
138 (2) INFORMATION FOR SEQ ID NO: 3:
140   (i) SEQUENCE CHARACTERISTICS:
141       (A) LENGTH: 441 amino acids
142       (B) TYPE: amino acid
143       (D) TOPOLOGY: linear
149   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
151 Met Thr Glu Glu Asn Lys Glu Leu Ala Asn Glu Leu Arg Arg Pro Pro

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152	1	5	10	15
154	Leu Cys Tyr	His Asn Gly Val	Gln Tyr Arg Asn Asn Glu Glu Trp Thr	
155		20	25	30
157	Asp Val Ser Cys Thr	Glu Cys His Cys Gln Asn Ser Val Thr Ile Cys		
158		35	40	45
160	Lys Lys Val Ser Cys Pro Ile Met Pro Cys Ser Asn Ala Thr Val Pro			
161		50	55	60
163	Asp Gly Glu Cys Cys Pro Arg Cys Trp Pro Ser Asp Ser Ala Asp Asp			
164	65	70	75	80
166	Trp Gly Ser Pro Trp Ser Glu Trp Thr Ser Cys Ser Thr Ser Cys Gly			
167		85	90	95
169	Gly Asn Ile Gln Gln Arg Gly Arg Ser Cys Asp Ser Leu Asn Asn Arg			
170		100	105	110
172	Cys Glu Gly Ser Ser Val Gln Thr Arg Thr Cys His Ile Gln Glu Cys			
173		115	120	125
175	Asp Lys Arg Phe Lys Gln Asp Gly Gly Trp Ser His Trp Ser Pro Trp			
176		130	135	140
178	Ser Ser Cys Ser Val Thr Cys Gly Asp Gly Val Ile Thr Arg Ile Thr			
179	145	150	155	160
181	Leu Cys Asn Ser Pro Ser Pro Gln Met Asn Gly Lys Pro Cys Glu Gly			
182		165	170	175
184	Glu Ala Arg Glu Thr Lys Ala Cys Lys Lys Asp Ala Cys Pro Ile Asn			
185		180	185	190
187	Gly Gly Trp Gly Pro Trp Ser Pro Trp Asp Ile Cys Ser Val Thr Cys			
188		195	200	205
190	Gly Gly Gly Val Gln Lys Arg Ser Arg Leu Cys Val Asp Ser Arg Met			
191		210	215	220
193	Thr Glu Glu Asn Lys Glu Leu Ala Asn Glu Leu Arg Arg Pro Pro Leu			
194	225	230	235	240
196	Cys Tyr His Asn Gly Val Gln Tyr Arg Asn Asn Glu Glu Trp Thr Val			
197		245	250	255
199	Asp Ser Cys Thr Glu Cys His Cys Gln Asn Ser Val Thr Ile Cys Lys			
200		260	265	270
202	Lys Val Ser Cys Pro Ile Met Pro Cys Ser Asn Ala Thr Val Pro Asp			
203		275	280	285
205	Gly Glu Cys Cys Pro Arg Cys Trp Pro Ser Asp Ser Ala Asp Asp Gly			
206		290	295	300
208	Trp Ser Pro Trp Ser Glu Trp Thr Ser Cys Ser Thr Ser Cys Gly Asn			
209	305	310	315	320
211	Gly Ile Gln Gln Arg Gly Arg Ser Cys Asp Ser Leu Asn Asn Arg Cys			
212		325	330	335
214	Glu Gly Ser Ser Val Gln Thr Arg Thr Cys His Ile Gln Glu Cys Asp			
215		340	345	350
217	Lys Arg Phe Lys Gln Asp Gly Gly Trp Ser His Trp Ser Pro Trp Ser			
218		355	360	365
220	Ser Cys Ser Val Thr Cys Gly Asp Gly Val Ile Thr Arg Ile Thr Leu			
221		370	375	380
223	Cys Asn Ser Pro Ser Pro Gln Met Asn Gly Lys Pro Cys Glu Gly Glu			
224	385	390	395	400

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226   Ala Arg Glu Thr Lys Ala Cys Lys Lys Asp Ala Cys Pro Ile Asn Gly
227                               405                               410                               415
229   Gly Trp Gly Pro Trp Ser Pro Trp Asp Ile Cys Ser Val Thr Cys Gly
230                               420                               425                               430
232   Gly Gly Val Gln Lys Arg Ser Arg Leu
233                               435                               440
235 (2) INFORMATION FOR SEQ ID NO: 4:
237   (i) SEQUENCE CHARACTERISTICS:
238       (A) LENGTH: 1326 base pairs
239       (B) TYPE: nucleic acid
240       (C) STRANDEDNESS: single
241       (D) TOPOLOGY: linear
247   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
249 ATGACTGAAG AGAACAAAGA GTTGGCCAAT GAGCTGAGGC GGCCTCCCCT ATGCTATCAC      60
251 AACGGAGTTC AGTACAGAAA TAACGAGGAA TGGACTGTTG ATAGCTGCAC TGAGTGTCAC      120
253 TGTCAGAACT CAGTTACCAT CTGCAAAAAG GTGTCCTGCC CCATCATGCC CTGCTCCAAT      180
255 GCCACAGTTC CTGATGGAGA ATGCTGTCCT CGCTGTTGGC CCAGCGACTC TCGCGACGAT      240
257 GGCTGGTCTC CATGGTCCGA GTGGACCTCC TGTTCTACGA GCTGTGGCAA TGAATTTCAG      300
259 CAGCGCGGCC GCTCCTGCGA TAGCCTCAAC AACCGATGTG AGGGCTCCTC GGTCCAGACA      360
261 CGGACCTGCC ACATTCAGGA GTGTGACAAA AGATTAAAC AGGATGGTGG CTGGAGCCAC      420
263 TGGTCCCCGT GGTTCATCTTG TTCTGTGACA TGTGGTGATG GTGTGATCAC AAGGATCCGG      480
265 CTCTGCAACT CTCCAGCCCC CCAGATGAAT GGGAAACCCT GTGAAGGCGA AGCGCGGGAG      540
267 ACCAAAGCCT GCAAGAAAGA CGCCTGCCCC ATCAATGGAG GCTGGGGTCC TTGGTCACCA      600
269 TGGGACATCT GTTCTGTCAC CTGTGGAGGA GGGGTACAGA AACGTAGTCG TCTCTGCGTC      660
271 GACTCTAGAA TGACTGAAGA GAACAAAGAG TTGGCCAATG AGCTGAGGCG GCCTCCCCTA      720
273 TGTATCACA ACGGAGTTCA GTACAGAAAT AACGAGGAAT GGAAGTGTGA TAGCTGCACT      780
275 GAGTGTCACT GTCAGAACTC AGTTACCATC TGCAAAAAGG TGTCTGCCCC CATCATGCCC      840
277 TGCTCCAATG CCACAGTTCC TGATGGAGAA TGCTGTCCTC GCTGTTGGCC CAGCGACTCT      900
279 GCGGACGATG GCTGGTCTCC ATGGTCCGAG TGGACCTCCT GTTCTACGAG CTGTGGCAAT      960
281 GGAATTCAGC AGCGCGGGCC CTCCTGCGAT AGCCTCAACA ACCGATGTGA GGGCTCCTCG     1020
283 GTCCAGACAC GGACCTGCCA CATTGAGGAG TGTGACAAAA GATTAAACA GGATGGTGCC     1080
285 TGGAGCCACT GGTCCCCGTG GTCATCTTGT TCTGTGACAT GTGGTGATGG TGTGATCACA     1140
287 AGGATCCGGC TCTGCAACTC TCCAGCCCC CAGATGAATG GGAAACCCTG TGAAGGCGAA     1200
289 GCGCGGGAGA CCAAAGCCTG CAAGAAAGAC GCCTGCCCCA TCAATGGAGG CTGGGGTCCT     1260
291 TGGTCACCAT GGGACATCTG TTCTGTCACC TGTGGAGGAG GGGTACAGAA ACGTAGTCGT     1320
293 CTCTAA                                           1326
295 (2) INFORMATION FOR SEQ ID NO: 5:
297   (i) SEQUENCE CHARACTERISTICS:
298       (A) LENGTH: 6 amino acids
299       (B) TYPE: amino acid
300       (D) TOPOLOGY: linear
306   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
308   Met Tyr Ile Gly Ser Arg
309   1           5
311 (2) INFORMATION FOR SEQ ID NO: 6:
313   (i) SEQUENCE CHARACTERISTICS:
314       (A) LENGTH: 33 base pairs
315       (B) TYPE: nucleic acid
316       (C) STRANDEDNESS: single

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317         (D) TOPOLOGY: linear
323     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
325 GTCGACATGT ATATTGGTTC TCGTTAAGTC GAC
327 (2) INFORMATION FOR SEQ ID NO: 7:
329     (i) SEQUENCE CHARACTERISTICS:
330         (A) LENGTH: 25 amino acids
331         (B) TYPE: amino acid
332         (D) TOPOLOGY: linear
338     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
340 Met Tyr Ile Gly Ser Arg Gly Lys Ser Tyr Ile Gly Ser Arg Gly Lys
341 1           5           10           15
343 Ser Tyr Ile Gly Ser Arg Gly Lys Ser
344           20           25
346 (2) INFORMATION FOR SEQ ID NO: 8:
348     (i) SEQUENCE CHARACTERISTICS:
349         (A) LENGTH: 90 base pairs
350         (B) TYPE: nucleic acid
351         (C) STRANDEDNESS: single
352         (D) TOPOLOGY: linear
357     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
359 GTCGACATGT ATATTGGTTC TCGTGTAATAA GTTATATTGG TTCTCGTGGT AAAAGTTATA
361 TTGGTTCTCG TGGTAAAGT TAAGTCGACC
363 (2) INFORMATION FOR SEQ ID NO: 9:
365     (i) SEQUENCE CHARACTERISTICS:
366         (A) LENGTH: 13 amino acids
367         (B) TYPE: amino acid
368         (D) TOPOLOGY: linear
373     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
375 Met Leu Tyr Lys Lys Ile Ile Lys Lys Leu Leu Glu Ser
376 1           5           10
378 (2) INFORMATION FOR SEQ ID NO: 10:
380     (i) SEQUENCE CHARACTERISTICS:
381         (A) LENGTH: 54 base pairs
382         (B) TYPE: nucleic acid
383         (C) STRANDEDNESS: single
384         (D) TOPOLOGY: linear
390     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
392 GTCGACATGC TTTATAAGAA GATCATCAAG AAGCTTCTTG AGAGTTAAGT CGAC
394 (2) INFORMATION FOR SEQ ID NO: 11:
396     (i) SEQUENCE CHARACTERISTICS:
397         (A) LENGTH: 46 amino acids
398         (B) TYPE: amino acid
399         (D) TOPOLOGY: linear
405     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
407 Met Leu Tyr Lys Lys Ile Ile Lys Lys Leu Leu Glu Ser Gly Lys Ser
408 1           5           10           15
410 Leu Tyr Lys Lys Ile Ile Lys Lys Leu Leu Glu Ser Gly Lys Ser Leu
411           20           25           30
413 Tyr Lys Lys Ile Ile Lys Lys Leu Leu Glu Ser Gly Lys Ser

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/036,869

DATE: 02/07/2002

TIME: 11:11:07

Input Set : N:\Crf3\RULE60\10036869.raw

Output Set: N:\CRF3\02072002\J036869.raw

L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]

L:1531 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:43